

SEQ ID NO: 6	A33	1	W V G K M W P V L W T L C A V R V T Y D A I S V E T P Q D V L R A S S Q G K S V T L P C T Y H T S T S
SEQ ID NO: 1	40628	1	W G T K A Q V E R K L C L F I L A I L C S L A L G S V T V H S S E P E V R I P E
SEQ ID NO: 2	45416	1	W G I L L G L L L G H L T Y D T Y G R P I L E V P E S V T G P W K G D V N L P C T Y D P L
SEQ ID NO: 9	35638	1	W A R R S R H R L L L R Y L V Y A L G Y H K A Y G F S A P K D O Q V V T A V E
SEQ ID NO: 10	JAM	1	W G T E G K A G R K L L F L F T S W I L G S S L V Q G K G S V Y T A O S D V Q V P E
A33	51	S R E G L I Q W O K L L L T H T E R V V I W P F S N K N Y I H G E L Y K H A V S I S N H A E Q S D A	
40628	43	H N P V K L S C A Y S G F S S P R V E W K F D Q G D T T R L V C Y N N K I T A S Y E D D R V T F L P T	
45416	47	Q G Y T Q V L V K W L V Q R G S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H K V P G D V	
35638	43	Y Q E A I L A C K T P K K T V S S R L E W K K L G R S V S F Y Y Q Q T L Q G D F K H R A E K I D F	
JAM	42	W E S I K L T C T Y S G F S S P R V E W K F V Q G S T T A L V C Y N S Q I T A P Y A D R V T F S S S	
A33	101	S I T I D Q L T W A D O N G G T Y E C S Y S L . W S D L E G H T K S R Y A R L L Y L V P P S K	
40628	93	G I T F K S V T R E D T G T Y T C M V S E E G G N S Y G E V K Y K L I V L V P P S K	
45416	97	S I Q L S T L E M D D A R S H Y T C E V T W Q T P D G N Q V V R D K I T E L V Q K L S V S K P T V T	
35638	93	H I R I K N V T R S D A G K Y R C E V S A P S E G G N L E E D T Y T L E V L V A P A V	
JAM	92	G I T F S S V T R K D N G E Y T C M V S E E G G N Y G E V S I H L T Y L V P P S K	
A33	144	P E C G I E G E T I I G N N I Q L T C Q S K E G S P T P Q Y S W K R Y N I L N Q E O	
40628	135	P T V N I P S S A T I G N H A V L T C S E Q D G S P P S E Y T W F K D G I V M P T N . P K S T R A F	
45416	147	T G S G Y G F T V P Q G M R I S L O C Q A . G S P P I S Y I W Y K Q Q T N N Q E P	
35638	137	P S C E V P S S A L S G T V V E L R C Q D K E G N P A P E Y T W F K D G I R L L E N . P R L G S Q S	
JAM	134	P T I S V P S S V T I G N R A V L T C S E H D G S P P S E Y S W F K D G I S M L T A D A K K T R A F	

SEQ ID NO: 6	A33	186	...	PLAQPASGQPVSLLKNI	STDTSGYYICTSSNEEG...	TQFCNITY
SEQ ID NO: 1	40628	184	SNS	SYYLNPTT	GELVFDPLSASDITGEYSCEARN	TPKTSNAV
SEQ ID NO: 2	45416	188	...	IKVATLSTLLFKPAYIA	DSGSYFCTAKGAVGSEQHS	DIVKFVVKD
SEQ ID NO: 9	35638	186	TNS	SYTNTKT	SKLDTGEYSCEARN	SYG...
SEQ ID NO: 10	JAM	184	WNS	SFTIDPKS	GOLIFDPTAFTDSGEYYC	QANGY...
					QANGY...	TAWSEAA
A33	227	AVRSPSW	NYVALYYGIAVGVV	ALIIGI	YCCCCRGKDDNTEDKEDA..	
40628	228	RWEAVERN	NYGYIVAYLY	LLGILVFGIWFAYSRGHFD	RTKKGTS...	
45416	233	SSKLLKT	KTEAPTTWYPLKATSTV	WDWTTWDGYLG	TSAGPCKSL	
35638	230	WQYDOL	NSGIIAYVY	YVCGLGCVYAAQRKGYF	SKETSFQKS..	
JAM	228	HWDAVELN	YGGIVAVVLY	LLIFGVWFAYSRGYFET	TKKGTA...	
A33	275	RPNREAYEE	PPPEQLREL	EDDYRQEERQSTG	RESPPDHLDQ	
40628	275	SKKVIYSQPSARSEGEF	KOTSSFLV...	
45416	283	PVF	AILIISLCCM	YVFTWAYIIMLCRKT	SQAEHYYEAR...	
35638	277	NSSSKATTW	SEN	YQWLT	PIPALWKAAGGSRGQE	F...
JAM	276	GKKVIYSQPS	STRSEGEF	KOTSSFLV...

FIG.-1B

SEQ ID NO:1

Met	Gly	Thr	Lys	Ala	Gln	Val	Glu	Arg	Lys	Leu	Cys	Leu	Phe	Ile	Leu	Ala	Ile	Leu	Cys	Ser	Leu	Ala	Leu	Gly	Ser	Val	Thr																																												
1	5	10	15	20	25	30	35	40	45	50	55	60	65	70	75	80	85	90	95	100	105	110	115	120	125	130	135	140	145	150	155	160	165	170	175	180	185	190	195	200	205	210	215	220	225	230	235	240	245	250	255	260	265	270	275	280	285	290	295	299											
Gl	u	Trp	Lys	Phe	Asp	Gln	Gly	Asp	Thr	Thr	Arg	Leu	Val	Cys	Tyr	Asn	Asn	Lys	Ile	Thr	Ala	Ser	Tyr	Glu	Asp	Arg	Val	Phe	Leu	95	100	105	110	115	120	125	130	135	140	145	150	155	160	165	170	175	180	185	190	195	200	205	210	215	220	225	230	235	240	245	250	255	260	265	270	275	280	285	290	295	299
Arg	Ala	Phe	Ser	Asn	Ser	Ser	Tyr	Val	Leu	Asn	Pro	Thr	Thr	Gly	Glu	Leu	Val	Phe	Asp	Pro	Leu	Ser	Ala	Ser	Asp	Thr	Gly	Glu	Tyr	210	215	220	225	230	235	240	245	250	255	260	265	270	275	280	285	290	295	299																							
Ala	Ala	Val	Leu	Val	Ile	Leu	Lys	Val	Ile	Tyr	Ser	Ala	Arg	Asn	Val	Arg	Asn	Val	Gly	Val	Ile	Val	240	245	250	255	260	265	270	275	280	285	290	295	299																																				
Lys	Gly	Thr	Ser	Ser	Lys	Val	Ile	Tyr	Ser	Gln	Pro	Ser	Ala	Arg	Ser	Glu	Gly	Glu	Phe	Lys	Gln	Thr	Ser	Ser	Phe	Leu	Val	240	245	250	255	260	265	270	275	280	285	290	295	299																															

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FIG.-2

SEQ ID NO:2
 1 MGILLGILLL GHLLTVDITYGR PILEVPESVT GPWKGDVNLPL CTDPLQGTYT QVLYKWLVQR GSDPVTIFLR DSSGDHIIQQA KYQGRLHVSQH KVPGDVSQQL
 101 STLEMDDRSH YTCEVTVWQTP DGNQVVRDKI TELRVQKLSV SKPTVTTGSG YGFTVTPQGMR ISLQCQARGG PPISYIWWKQ QTRNQEPIKV ATLSTLLFKP
 ^Glycosaminoglycan attachment site

201 AVIADGSYF CTAKGQVGSE QHSIVKFWV KDSSKLLKTK TEAPTTMVTYK LKATSTVKQS WDWTTDMGY LGETSAGPGK SLPVFAIILI ISLCCMVVFT
Transmembrane domain

FIG._3

301 MAXIMLCKRT SQQEHVYEEAA R

OLI2166 (35936.f3)
 SEQ ID NO:16
 TTGCCTTACTCAGGTGCTAC

OLI2167 (35936.r2)
 SEQ ID NO:17
 ACTCAGCAGTGGTAGGAAAG

OLI2162 (35936.f1)
 SEQ ID NO:12
 TCGCGGAGGCTGTGTTCTGTTTCCC

OLI2163 (35936.p1)
 SEQ ID NO:13
 TGATCGCGATGGGACAAAGGGCAAGCTCGAGAGGAAACTGTTGTGCCT

OLI2164 (35936.f2)
 SEQ ID NO:14
 ACACCTGGTTCAAAGATGGG

OLI2165 (35936.r1)
 SEQ ID NO:15
 TAGGAAGAGTTGCTGAAGGCACGG

FIG._8

DNA35936 SEQ ID NO:3

CTTCTTGCCA ACTGGTATCA CCTTCAAGTC CGTGACACGG GAAGACACTG 50
 GGACATACAC TTGTATGGTC TCTGAGGAAG GCGGCAACAG CTATGGGAG 100
 GTCAAGGTCA AGCTCATCGT GCTTGTGCCT CCATCCAAGC CTACAGTTAA 150
 CATCCCCCTCC TCTGCCACCA TTGGGAACCG GGCAGTGCTG ACATGCTCAG 200
 AACAAAGATGG TTCCCCACCT TCTGAATACA CCTGGTTCAA AGATGGGATA 250
 GTGATGCCTA CGAATCCCAA AAGCACCCGT GCCTTCAGCA ACTCTTCCTA 300
 TGTCCCTGAAT CCCACAACAG GAGAGCTGGT CTTTGATCCC CTGTCAGCCT 350
 CTGATACTGG AGAATACAGC TGTGAGGCAC GGAATGGGTA 390

FIG._4A

consen01 SEQ ID NO:4

TCTCAGTCCC CTCGCTGTAG TCGCGGAGCT GTGTTCTGTT TCCCAGGAGT 50
 CCTTCGGCGG CTGTTGTGCT CAGGTGCGCC TGATCGCGAT GGGGACAAAG 100
 GCGCAAGCTC GAGAGGAAAC TGTTGTGCCT CTTCATATTG GCGATCCTGT 150
 TGTGCTCCCT GGCATTGGC AGTGTACAG TTGCACTCTT CTGAACCTGA 200
 AGTCAGAATT CCTGAGAATA ATCCTGTGAA GTTGTCTGT GCCTACTCGG 250
 GCTTTCTTC TCCCCGTGTG GAGTGAAGT TTGACCAAGG AGACACCACC 300
 AGACTCGTT GCTATAATAA CAAGATCACA GCTTCCTATG AGGACCGGGT 350
 GACCTTCTTG CCAACTGGTA TCACCTTCAA GTCCGTGACA CGGGAAAGACA 400
 CTGGGACATA CACTTGTATG GTCTCTGAGG AAGGCGGCAA CAGCTATGGG 450
 GAGGTCAAGG TCAAGCTCAT CGTGCTTGTG CCTCCATCCA AGCCTACAGT 500
 TAACATCCCC TCCTCTGCCA CCATTGGAA CCGGGCAGTG CTGACATGCT 550
 CAGAACAAAGA TGGTTCCCCA CCTTCTGAAT ACACCTGGTT CAAAGATGGG 600
 ATAGTGATGC CTACGAATCC CAAAAGCACC CGTGCCTTCA GCAACTCTTC 650
 CTATGTCCTG AATCCACAA CAGGAGAGCT GGTCTTGAT CCCCTGTCAG 700
 CCTCTGATAAC TGGAGAATAC AGCTGT 726

FIG._4B

consen02 SEQ ID NO:5

GCAGGCCAAAG TACCAGGGCC GCCTGCATGT GAGCCACAAG GTTCCAGGAG 50
 ATGTATCCCT CCAATTGAGC ACCCTGGAGA TGGATGACCG GAGCCACTAC 100
 ACGTGTGAAG TCACCTGGCA GACTCCTGAT GGCAACCAAG TCGTGAGAGA 150
 TAAGATTACT GAGCTCCGTG TCCAGAAACT CTCTGTCTCC AAGCCCACAG 200
 TGACAACCTGG CAGCGGTTAT GGCTTCACGG TGCCCCAGGG AATGAGGATT 250
 AGCCTTCAAT GCCAGGGTTC GGGGTTCTCC TCCCATCAGT TATATTGGT 300
 ATAAGCAACA GACTAATAAC CAGGGAACCC ATCAAAGTAG CAACCTAAG 350
 TACCTTACTC TTCAAGCCTG CGGTGATAGC CGACTCAGGC TCCTATTCT 400
 GCACTGCCAA GGGCCAGGTT GGCTCTGAGC AGCACAGCGA CATTGTGAAG 450
 TTTGTGGTCA AAGACTCCTC AAAGCTACTC AAGACCAAGA CTGAGGCACC 500
 TACAACCATG ACATACCCCT TGAAAGCAAC ATCTACAGTG AAGCAGTCCT 550
 GGGACTGGAC CACTGACATG GATGGCTACC TTGGAGAGAC CAGTGCTGGG 600
 CCAGGAAAGA GCCTGCCTGT CTTGCCATC ATCCTCATCA TCTCCTTGTG 650
 CTGTATGGTG GTTTTACCA TGGCCTATAT CATGCTCTGT CGGAAGACAT 700
 CCCAACAAAGA GCATGTCTAC GAAGCAGCCA GGGCACATGC CAGAGAGGCC 750
 AACGACTCTG GAGAAACCAT GAGGGTGGCC ATCTTCGCAA GTGGCTGCTC 800
 CAGTGATGAG CCAACTTCCC AGAATCTGGG GCAACAACTA CTCTGATGAG 850
 CCCTGCATAG GACAGGAGTA CCAGATCATC GCCCAGATCA ATGGCAACTA 900
 CGCCCCGCTG CTGGACACAG TTCCTCTGGA TTATGAGTTT CTGGCCACTG 950
 AGGGCAAAAG TGTCTGTTAA AAATGCCCA TTAGGCCAGG ATCTGCTGAC 1000
 ATAATTGCCT AGTCAGTCCT TGCCTTCTGC ATGGCCTTCT TCCCTGCTAC 1050
 CTCTCTTCCCT GGATAGGCCA AAGTGTCCGC CTACCAACAC TGGAGCCGCT 1100
 GGGAGTCACT GGCTTGCCC TGGAAATTGC CAGATGCATC TCAAGTAAGC 1150
 CAGCTGCTGG ATTTGGCTCT GGGCCCTTCT AGTATCTCTG CCGGGGGCTT 1200
 CTGGTACTCC TCTCTAAATA CCAGAGGGAA GATGCCATA GCACTAGGAC 1250
 TTGGTCATCA TGCCTACAGA CACTATTCAA CTTGGCATC TTGCCACCAG 1300
 AAGACCCGAG GGGAGGCTCA GCTCTGCCAG CTCAGAGGAC CAGCTATATC 1350
 CAGGATCATT TCTCTTCTT CAGGGCCAGA CAGCTTTAA TTGAAATTGT 1400
 TATTCACAG GCCAGGGTTC AGTTCTGCTC CTCCACTATA AGTCTAATGT 1450
 TCTGACTCTC TCCTGGTGCT CAATAAATAT CTAATCATAA CAGCAAAAAA 1500
 AAA 1503

FIG._4C

SEQ ID NO:11 CGAGGTCCCTT CGGGGGCTGT TGTGTCACTG GCCTGATCGC GATGGGGACA AAGGGCAAG TCGAGAGGA ACTGTTGTGC CTCTTCATAT 100
 TGGGGATCCT GTGTGCTCC CTGGCATTGG GCACTCTAC AGTGCACCTCT TCTGAACTCT AAGTCAGAAAT TCTGAGAAAT AATCCCTGTAA AGTGTGTCCTG 200
 TCCCTACTCG GGCTTTCTT CTCCCCGTGT GGAGTGGAAAG TTTGACCAAG GAGACACCAC CAGACTCGTT TGCTATAATA ACAAGATCAC AGCTTCCTAT 300
 GAGGACGGG TGACCTTCTT GCCAACTGGT ATCACCTCA AGTCCCGTGC ACAGGGAGAC ACTGGGACAT ACACCTGTAT GGTCTCTGAG GAAAGGGGGCA 400
 ACAGCTATGG GGAGGTCAAG GTCAAGGTCA TCGTGCCTGT GCCTCCATCC AAGCCTACAG TAAACATCCC CTCTCTGCC ACCATTGGGA ACCGGGGAGT 500
 GCTGACATGC TCGAGAACAG ATGGTCCCC ACCTTCTGAA TACACCTGGT TCAAAGATGG GATACTGTGC CCTACGAATC CCAAAGCAC CGGTGCCCTC 600
 AGCAACTCTT CCTATGTCTT GAATCCACCA ACAGGAGAGC TGGTCTTGA TCCCCTGTCA GCCTCTGATA CTGGAGAATA CAGCTGTGAG GCACGGAAATG 700
 GGTATGGAC ACCCATGACT TCAAATGCTG TCGGGCATGGA AGCTGTGGAG CGGAATGTGG GGCTCATCGT GGCAAGCCGTC CTGGAAACCC TGATTCTCCT 800
 GGGAAATCTTG GTTTTGGCA CTATAGCCGA GGGCACTTGT ACAGAACAAA GAAAGGGACT TCGAGTAAGA AGGTGATTTA CAGCCAGCCT 900
 AGTGCAGGAA GTGAAGGAGA ATTCAGAACAG ACTCTGTCAT TCCTGGTGTG AGCCTGGTGC GCTCACCGGCC TATCCTCTGC ATTGCCCTTA CTCAAGGGCT 1000
 ACGGGACTCT GCCCCCTGTAT GTCTGTAGTT TCAAGGATG CCTTATTTGT CTCTTACAC CCACAGGGCC CCTACTTCT TCGGATGTGT TTTAATAAT 1100
 GTCAGGCTATG TGCCCCATCC TCCTTCATGCC CCTCCCTCCC TTTCCTACCA CTGCTGAGTG GCCTGGAACT TGTTAAAGT GTTAACTCCC CAATTCCTTG 1200
 AGGGATCAGG AGGAATCTCTT GGGTATGCCA TTGACTCTCCC TTCTAAGTAG ACAGCAAAA TGGGGGGGT CGCAAGGAAAT TGCACCTCAAC TGCCCACCTG 1300
 GCTGGAGGG ATCTTGAAT AGGTATCTTG AGCTGGGTC TGGGCTCTT CCTGTGTAC TGACGACCA TGCTGGCTGT TCTAGAGGG GAAATTAGGG 1400
 CTAGAGGGCC TGAATGGT GTTGTGTAT GACACTGGG TCCTTCATC TCTGGGGCC ACTCTCTCT GTCTTCCCAT GGGAAAGTGC ACTGGGATTC 1500
 CTCTGCCCC TGCAAGCTGA TACAAGCTGA CTGACATTGA CTGCTGCTGT GGAAATGGG AGCTCTGT GTGGAGAGCA TAGTAAATT TGAGAGAACT 1600
 TGAAGCCAA AGGATTAA ACCGCTGCTC TAAAGAAAG AAAACTGGAG GCTGGCTCAGG CCTGTAATCC CAGGGCTGA GGCAGGGGGAA 1700
 TCACCTGAGG TCGGGAGTC GGGATCAGCC TGACCAACAT GGAGAAACCC TACTGGAAAT ACAAACTTAG CGAGGCATG TGTTGCATGC CTGTAGTCCC 1800
 AGCTGCTCAG GAGCCTGGCA ACAAGAGCAA AACTCCAGCT CA 1842

SEQ ID NO:7

1 CCCACCCGTC CGCCCCACGG TCCCCCACCG GCTCCCCCA CCCGCTCCCCG CCACCAAGAAG TTTGCTCCCTC TTTGCTACCA GGAGGGCTGGA AGAAACGACA
GGGTGGCGAG GGGGGTCCGC AGGGGGTCCG

101 GAACTAGCTC TCCCCTGTGAT CGGGATCTTA CTGGGGCTGCC TACTCTCTGG CCACCTAACAA GTGGACACTT ATGGCCGCTCC CATCCCTGAA GTCCCCAGAGA
CTTCATCGAG ACCGACACTA CCCCTAGAAT GACCCGGACCC ATGAGGACCC CGTGGATTTGT CACCTGTGAA TACCGCAGG GTAGGACCTT CACGGTCTCT
1 SEQ ID NO:2 M C I L L G L L C H L T V D T Y G R P I L E V P E S
~MET

201 GTGTAAACAGG ACCCTTGAAA CGGGATGTCATCTG CACCTATGAC CCCCTGCAAG GCTACACCCA AGTCTTGTCG AAGGGCTGG TACAACGTCG
CACATGTCCTC TGGAACCTTT CCCCTACACT TAGAAGGGAC CTGGCATACTG GGGGACCTTC CGATGTCGCT CAGAACCCAC TTCAACGGACC ATGGTGGACCC
29 V T G P W K G D V N L P C T Y D P L Q G Y T Q V L V K W L V Q R G

301 CTCAAGACCTT GTCACCATCTT TTCTACTGTGA CTCTTCTGGAA GACCATATCC ACCGATATCC GTACCAAGAAA GTACCAAGGGC CGCCCTGCATG TGACCCACAA CGTTCACAGGA
GACTCTGGGA CACTGGTAGA AAGATGCACT GAGAAGACCT CTGGTATAGG TCCTGCTGGTT CATGGTCCC CGGGACGTAC ACTGGTCTT CCAAGGTCT
62 S D P V T I F L R D S S G D H I Q Q A X Y Q G R L H V S H K V P G

401 GATGTATCCC TCCAATTGAG CACCCCTGGAG ATGGATGACCC GGAGGCCACTA CACGGTGTGAA GTCACCTGGC AGACTCTGTA TCCCAACCAA GTCGTGAGAG
CTTACATAGGG AGCTTAACCTC GTGGGACCTC TACTACTGG CCTCTGGTGTAT GTGCAACACTT CACTGGACCC TCTGAGGACT ACCGGTGGTT CAGCACTCTC
95 D V S L Q L S T L E M D D R S H Y T C E V T W Q T P D G N Q V V R D

501 ATTAAGATTTAC TGACCTCCGT GTCCAGAAAC TCTCTGTCTC CAAGCCCCACA GTGACMACTG GCAGGGGTTA TGGCTTCACG GTCCCCCAGG GAATGAGGAT
TATTCTTAATG ACTCGAGGCA CAGGTCTTTC AGAGACAGAG GTTCGGGGTGT CACTGTTGAC CGTGGCCAAAT ACCGAAAGTGC CACGGGTCC CTTAACTCTA
129 K I T E L R V Q K L S V S K P T V T T C S C Y G F T V P Q G M R I

601 TAGCCCTCAA TGGCAGGCTC GGGGTTCTCC TCCCATCACT TATATTGGT ATAAACCAACA GACTAAATAAC CAGGAACCCA TCAAAGTACCC AACCCCTAAGT
ATCGGAAAGTT ACGGTCCGAG CCCCAAGAGG AGGTAGTCA ATATAACCA TATTCTGGTT CTGATTATTG GTCCTTGGGT AGTTTCATCG TTGGGGATTCA
162 S L Q C Q A R G S P P I S Y I W Y K Q Q T N N Q E P I K V A T L S

FIG.- 6A

SEQ ID NO:7 701 ACCCTTACTCT TCAAGCCTGG CGTGATAGCC GACTCAGGCT CCTATTCTG CACTGCCAAG GGGCAGGTTG CCTCTGACCA GCACAGGAC ATTGTGAAGT
TGGAAATGAGA AGTTCGGAGC CCACTATGG CTCAGCTGG CGNTAAAGAC GTGACGGTT CCGGTCAC ACAGACTCTGT CGTGTGCTG TAACTCTCA

SEQ ID NO:2 195 T L L F K P A V I A D S C S Y F C T A K G Q V G S E Q H S D I V K F
801 TTGTGGTCAA AGACTCCTCA AGACTACTCA AGACCAAGAC TGACCCACCT ACAACCATGA CATAACCCCTT GAAAGAACAA TCTACAGTGA AGCAGTCTGT
AACACCAGTT TCTCAGGACT TTCTGATGAGT TCTGGCTCTG ACTTCCGGAA CTATCCCTACT GTTCTGGTT AGATGTCACT TCGTCAGGAC

229 V V K D S S K L L K T K T E A P T T M T Y P L K A T S T V K Q S W
901 GGACTGGACC ACTGACATGG ATGGCTTACCT TGGAGAGGCC AGTCTCTGGG CAGGAGAG CAG CCTGCTGTGC TTTGCCATCA TCCTCATCAT CTCCTGTGC
CCTGACCTGG TGACTGTACC TACCGATGCA ACCTCTCTGG TCACGAGCCGG GTCCCTTCTC GCACCCAGAG AACGGTAGT AGGAGTAGTA GACGGACAG
262 D W T T D H D G Y L G E T S A G P K S L P V F A I I L I I S L C

1001 TCTATGGTCC TTTTACCAT CCCCTATATC ATGCTCTGTC CGAGAGATC CCAACAGAG CATGCTCTAG AGGAGCCAG GTAGAAAGT CTCTCCTCTT
ACATACCCAC AAAATGGA CGGGATATAG TACCGATAG CCGGAGAC CCTTCTCTAG GGTTGTTCTC GTACAGATGC TTCTGTCGGTC CATTCTTCA GAGAGGAGAA
295 C H V V F T M A Y I H L C R K T S Q Q E H V Y E A A R O

1101 CCATTTTGA CCCCTCCCT CCCCTCAATT TTGATTACTG CGAGGAAAGG TGGAGATG TGAGGAAAGG GGGGTGTGGC ACAGACCAA TCCTAAGGGC GGAGGCTTC
GGTAAAACCT GGGCAGGGA CGGGCAGGAA AACTATGAC CCTCCCTTAC ACCTCCCTTC ACCTCCCTAC GCTCTGGTT AGGATTCCCG CCTCCGGAAAG
1201 AGGGTCAGGA CATAGCTGCC TTCCCTCTCT CAGCCACCTT CTGAGGTTGT TTTGGCCCTC TGAAACACAA CGATAATTAA GATCCATCTG CCTCTGCTT
TCCCAGTCT GTATGGACGG AAGGGAGAGA GTCCGTGGAA GACTCCAAACAA AAACCGGGAG ACTTCTGTT CCTATTAAAT CTAGGTAGAC GGAAAGACCAA

1301 CCAGATCCC TGGGGTAG GATCCGTATA ATTAAATGCC AAGAAATGAG CCAGNAGGCT GGGAAACAG GACCAACGCC CCAAGTCCCT TCTTATGGT
GGTCTTGGG ACCCACCACCT CTAGGACTAT TAATAACCG TTCTTAACCT CGTCTTCCCA CCCTTGGTC CTGGTGTGG CGTTCAAGGA AGATAACCA

1401 GGTGGCTCT TGGCCCATAG GGCACATGCC AGAGAGGCC ACCACTCTGG AGAAACCATG AGGGGGCCA TCTTCGAAAG TGGCTGCTCC AGTGTGAGC
CCACCCGAGA ACCCGTATC CGGTGTACGG TCTCTCCGT TCCTAGACCC TCCCTGGTAC TCCCTAGAC TCCCTAGAC TCCCTAGAC

1501 CAACTTCCA GAATCTGGEC ACAACTACT CTGATGAGCC CTGGCATAGGA CAGGAGTAC AGATCATCCC CAGATCAAT GGAAACTACG CCCGCTGCT
GTTGAAGGGT CTAGACCCG TTGTTGATGA GACTACTCG GACGTATCCCT CTCTCTATGG TCTAGTAGGG CGTCTAGTTA CCCTTGTATGC CGTCTAGTTA

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FIG.-6B

SEQ ID NO:7

1601 GGACACAGT CCTCTGGATT ATGACTTTCT CCCCACTGAG GGCAAAAGTC TCTGTTAAA ATGCCCATTT AGCCAGGAT CTGCTGACAT AATTGCCCTAG CCTCTGTCAA CGAGACCTAA TACTCAAAGA CGGTGACTC CCGGTCAAC AGACATTTT TACGGGGTAA TCCGGTCTA GACGACTGTA TAAACGGATC

1701 TCAAGCCTG CCTCTGGAT CCCCTCTTC CCTGCTACCT CTCTTCTGG ATAGCCCCAA GTGTCGGCCCT ACCAACACTG GACCCGCTGG GAGTCAGTG ACTCAGAAC CGAAGACGTAA CGGAAGAAC GGACGATGGA GAGAAGGACCTT CACAGGGGAA TATCGGGTTT CGACGACTC TCTGGGACCT CTCAGTGAC

1801 CTTTGCCTG GAATTGCCA GATGGCATCTC AAGTAAGCCA GCTGCTGGAT TTGGCTCTGG CCCCTCTAG TATCTCTGCC GGGGCTTCT GGTAACCTCTC GAAACGGGAC CTTAAACGGT CTACGTAGAG TTCAATTGGT CGACGACTA AACCGAGACC CGGAAGATC ATAGAGACGG CCCCGAAGA CCATGAGCAG

1901 TCTAAATACC AGACGGAAAGA TGCCCCATAGC ACTAGGACTT GGTCTATCATG CCTACAGACA CTATTCAGT TTGGCATCTT CCCACAGAA GACCCGAGCC AGATTTATGG TCTCCCTCTC ACGGGTATCG TGATCCTGAA CCAGTAGTAC CGATGCTCTGT GATAAGTGA AACCGTAGAA CGGGGCTTCTT CTGGGGCTCC

2001 AGGGTCAGCT CTGCCAGCTC AGAGGACCCAG CTATATCCAG GATCATTTCT CTTTCTTCAG GCCCAGACAG CTTTTAATTG AATTTCTTAT TTCAACGGCC TCCCGACTGA GACGGTCAG TCTCCTGGTC GATATAGCTC CTACTAAAGA GAAGGAAGTC CGGGTCTGTC GAAATTAAC TTAACAATA AAGTGTCCGG

2101 AGGGTCAGT TCTGCTCCTC CACTATAAGT CTMAGTGTCTT GACTCTCTCTC TGCTGCTCAA TAAATATCTA ATCATAACAG C TCCCAAGTCA AGACGGGGAG ACCACGAGTT ATTACACAGA CTGAGAGAGG GATGATATTCA GTGATATTCA ATTATAGAT TACTATGTC G

FIG.-6C

SEQ ID NO:8

CCAGAGTTCAAGGGCCCCGGCTCCTGCGCTCCTGCCGCCGGGACCCCTGACCTCCT
 CAGAGCAGCCGGCTGCCGCCGGGAGATGGCGAGGAGGCCACCGCCTCCTCCT
 GCTGCTGCGCTACCTGGTGGTCGCCCTGGCTATCATAAGGCCTATGGGTTTCTGC
 CCCAAAAGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTAGCCTGCAA
 AACCCCAAAGAAGACTGTTCTCCAGATTAGAGTGGAAAGAAACTGGGTGGAGTGTCTC
 CTTGTCTACTATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGA
 TTTCAATATCGGATCAAAATGTGACAAGAAGTGTGAGCTGGGAAATATCGTTGTGAAGT
 TAGTGCCCCATCTGAGCAAGGCCAAACCTGGAAAGAGGATACTGCACTCTGGAAAGTATT
 AGTGGCTCCAGCAGTCCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGT
 AGAGCTACGATGTCAAGACAAAGAAGGGATCCAGCTCCTGAATACACATGGTTAAGGA
 TGGCATCCGTTGCTAGAAAATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACAC
 AATGAATACAAAAACTGGAACTCTGCAATTAAACTGTTCCAAACTGGACACTGGAGA
 ATATTCTGTGAAGCCCGCAATTCTGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCA
 AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCCGTAGTAGTTGTGGCCTAGTGAT
 TTCCGTTGTGGCCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTCAAAAGAAAC
 CTCCCTCCAGAAGAGTAATTCTCATCTAAAGCCACGACAATGAGTAAAATGTGCAGTG
 GCTCACGCCTGTAATCCCAGCACTTGGAAAGGCCGCGGGGGATCACGAGGTCAGGA
 GTTCTAGACCAGTCTGGCCAATATGGTGAACCCCCATCTACTAAAATACAAAAATTAG
 CTGGGCATGGTGGCATGTGCCTGCAGTCCAGCTGCTGGGAGACAGGAGAATCACTTGA
 ACCCGGGAGGCAGGTTGCAGTGAGATCACGCCACTGCAGTCCAGCCTGGTAA
 CAGAGCAAGATTCCATCTCAAAAATAAAATAAAATAACTGGTTTAC
 TGTAGAATTCTTACAATAATAGCTTGATATT

FIG._7

SEQ ID NO:9

MARRSRHRLLLLLRLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKT
 LEWKKLGRSVSFVYYQQLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN
 LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNP
 PAPEYTWFKDGIRLLENPR
 LGSQSTNSSYT
 MNTKTGTLQFNTVSKLDTGEYSCEARN
 SVGYRRCPGKRMQVDDLN
 ISGI
 IAAVVVALVIS
 VCGLGV
 CYAQRKGYFSKETSFQKS
 NSSSKATT
 MENVQWL
 T
 P
 V
 I
 P
 A
 L
 W
 KAAAGGSRGQEF

FIG._11

SEQ ID NO:5

1 GCACCCCAAG TACCCAGGGCC GCTTCCATGT GAGCCACAG GTTCCAGGAG ATGTATCCCT CCATTTGAGC ACCCTGGAGA TGGATGACCC GACCCACTAC
CCTCCCTTC ATGGTCCCGG CGGACGTACA CTCGGTCTC CTGGCTGAGA TACATAGGA GGTTACCTCG TGGGACCTCT ACCTACTGGC CTCGGTGATG
~42257. f1 SEQ ID NO:18 ~42257. p1 SEQ ID NO:22

101 ACCTGTGAAG TCACCTCCCA GACTCCTGAT CCCAACCAAC TCGTGGAGA TAAGATTACT GAGCTCCGTG TCCAGAACT CTCTGTCTCC AACCCACAG
TGGACACTTC ACTGGACCCG CTGAGGACTA CGGTGGTTC ACCACTCTCT ATTCTAATGA CTTCAGGAGA AGGTCTTGA GAGACAGGG TTGGGTGTC
~42257. f1 SEQ ID NO:18

201 TGCACAACTGG CAGGGGTAT GGCCTCACCG TGCCCCAGG AATGAGGATT AGCCTTCAT CCCAGGGTTC CGGGTTCTCC TCCCATCACT TATATTGGT
ACTGTGTGACCG GTGGCCAAATA CGGAAAGTGGC ACCGGGTCTC TTACTCTTA CGCCAACTTA CGGTCCCAAG CCCAAAGAGG AGGGTACTA ATATAAACCA
~42257. f1 SEQ ID NO:18

301 ATAAGGCAACA GACTAATAAC CAGGGAAACCC ATCAAAGTAG CAAACCTAAAG TACCTTACTC TTCAAGGCTG CGGTGATACC CGACTCAGGC TCCTATTCT
TATTGTTGTT CTGATTATTG GTCCTCTGG TAGTTTCATC GTGGGATTG ATGGAAATGAG AAGTTGGAC GCACTATCG CCTGAGTCGG AGGATAANGA
~42257. f1 SEQ ID NO:18

401 GCACTGCCAA GGGCCACCTT GGCCTCTGAG ACCACAGGA CATTGTGAAG TTGTGGTCA AAGACTCTTC AAAGCTACTC AAGACCAACA CTGACGGCACC
CCTGACCCCTT CCCCTCCAA CGGAGACTCG TCGTGTCCCT CTAAACACTTC ANACCCAGT TTCTGTGAG TTTCGTGAG TTCTGGTCTC GACTCGTGC
~42257. f1 SEQ ID NO:20

501 TACAACCATG ACATACCCCT TGAACCAAC ATCTACAGTG AAGCAGCTCTT GGGACTGGAC CACTGACATG GATGGCTTACG TTGGAGAGAC CAGTGTGG
ATGGTTGGTAC TGTATGGGA ACTTTCGTTG TAGATGTCAC TTTCGTCAGGA CCTTGACCTG GTGACTCTAC CTACCGATGG AACCTCTCTG GTCACGACCC
~42257. f1 SEQ ID NO:20

601 CAGGAAAGA GCCTGGCTGT CTTGCCATC ATCCTCATCA TCTCCCTGTG CTGTATGGTG GTTTTACCA TGGGCTTAT CATGGCTCTGT CGGAAGACAT
GCTCCCTTCCT CGGACGGACA GAAACGGTAG TAGGAGTAGT AGAGGAACAC GACATACCAAC CAAAAATGGT ACCGGATATA GTACCGACCA GCCTTCTGTA
~42257. f2 SEQ ID NO:19

701 CCCAACAAAGA GCATGTCTAC GAAGCAGGCCA CGGCCACATGC CAGAGGGCC AACGACTCTG GAGAACCAT GAGGGTGGCC ATCTTCGCAA GTGGCTGCTC
GGGTGGTCTCT CGTACAGATG CTTGCTGGT CCCGTGTAGC GTCTCTCCGG TTGCTGAGAC CTCTTGGTA CTCCCACGG TAGAAGGGT CACCGACGAG
~42257. f2 SEQ ID NO:19

FIG.- 9A

SEQ ID NO:5

801 CAGTGATGAG CCAAATCTCCC AGAATCTGGG CCACACACTA CTCTGATGAG CCCTGCATAG CACAGGAGTA CCAGATCATC CCCAGATCA ATGCCAACTA
GTCACATCTC CGGTGAAGGG TCTTAGACCC CGTTCTGAT GAGACTACTC GGGACGTATC CTGTCCTCAT CGTCTAGTAG CGGTCTAGT TACCGTTGAT

901 CGCCCCCTG CTGGACACAG TTCCCTCTGCA TTATGAGTTT CTGGCCACTG AGGGCAGAG TGTCTGTTAA AAATGCCCA TTAGGCCAGG ATCTGGCTGAC
GGGGGGGAC GACCTGTGTC AAGGAGACCT ANTACTAAA GACCGGTAC TCCCCGTTTC ACAGACAATT TTACGGGT AAACGGTCC TAGACGACTG

1001 ATAAATGGCT AGTCAGTCCT TGCCTCTGC ATGGCTTCTC TCCCTGCTAC CTCTCTTCTC CTGATGCCA AGTGTCCGC CTACCAACAC TGGAGCCGCT
TATTAACGGA TCACTCAGGA ACGGAAGACG TACGGGAGA AGGGACGATG GAGAGAAGGA CCTATGGGT TTACACAGGG GATGGTTGTG ACCTCGGGGA

1101 GGGAGTCATC GGTTGGCC TGGAATTGTC CAGNTCCATC TCAAGTAAAGC CACCTCTGG ATTTCGCTCG GGGCCCTCT AGTATCTCTG CGGGGGGCTT
CCCTCACTGA CGGAAACGGG ACCTTAACCG GTCTACGTTAG AGTTTCACTGG GTCGACGACC TAACCCGAGA CCCGGGAAGA TCATAGAGAC GCCCCCGAA

^42257.r2 SEQ ID NO:21

1201 CTGGTACTCC TCTCTAAATA CCAGGGGA GATCCCCATA GCACTAGGAC TTGGCTCATCA TCCTCTACAGA CACTATTCA CTTGGCCATC TTGCCACAG
GACCATGAGG AGAGATTAT CGTCTCCCT CTACGGTAT CGTGATCTC AACCAGTACT ACCCATGTC GTGATAAGT GAAACCGTAG AACCTTAACA

1301 AAGACCCGAG GGAGGGCTCA CCTCTGGCAG CAGCTATTC CAGGATCATT TCTCTTTCTT CAGGGCAGA CAGCTTTAA TTGAAATTCT
TTCTGGCTC CCCTCCGAGT CGAGACGTC GACTCTCTG GTCGATATAG GTCCTACTAA AGAGAAAGAA GTCGGAAATT AACCTTAACA

1401 TATTACAG GCGAGGGTTC AGTTCTCTC CTCCACATA AGTCTAATGT TCTGACTCTC TCCTGGTGTGCT CAATAATAT CTAACTAA CAGCAAAAGA
ATAAAAGTGTC CGGTCCAAAG TCAAGACGAG GAGGTGATAT TCAGATTACA AGACTGAGAG AGGACACGA GTTATTATA GATTAGTATT GTCGTTTTTT

1501 AAA
TTT

FIG._ 9B

A33 HUMAN A33 ANTIGEN PRECIB/SOB - HOMO SAPIENS

A33 HUMAN - A33 ANTIGEN PRECUBBSOB : HOMO SAPIENS (319 aa)

SCOPE = 316 (86 6 BITS) EXPECT = 380-19 P = 280-19

SCORE = 240 (00:00:00); LNK

DNA40628 121 LALGSVTVHSSEPEVRIPENNPKLSCAYSGFSSPR-- -VEW- KFDQGDTTRLVC--YNN
IDENTIES = 81/268 (30%), POSITIVE = 131/268 (48%), ALIGNED, FRAME = +1

SEQ ID NO:23

A33_human 17 VTVDAISVETPQDVLRASQGKSVTLPCYHTSTSREGLIQWDKLLLTHTERVVWPFNSN
SEQ ID NO:24

DNA40628	283	K--ITAS-YEDRVTFL-----PTGITEFKSVTREDTGTYTCMVS---EEGGNSYGEVKVK
		* * * . * . * * . * * * * * . * * . * * . * . * . * .
A333	human	77 KNYIHGELYKKNRVSISNNAE OSDASITIDQLTMADNGTYECVSLSMSDLEGNT - KSRVR

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FIG. 10A

SCORE = 245 (86.2 BITS), EXPECT = 3.6e-19, P = 3.6e-19
IDENTITIES = 83/273 (30%), POSITIVES = 131/273 (47%), AT 1112,12, FRAME = +1

DNA40628	112	LCSL--ALGSVTVHSSEPEVRIPENNPKVLSAYSGFSSPR---VEW-KFDQGDTTRVC
SEQ ID NO:25		* * * * * * * * *
A33 human	12	LCAVRVTVDAAISVETPQDVLRASQGKSVTLPCTYHTSTSREGLIQWDKLLLTERVVI
SEQ ID NO:26		

DNA4 0628	274	- - YNNK -- ITAS - YEDRTVTL - - - - PTGIFTFKSVTREDTGTYTCMVSEEGNNSYGEVK
	.	• * * * * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * .
A33	human	72 WPFESNKNYIHEGELYKNRVSISNNAEQSDASITIDQILTMDNGTYECSVSLMS - DLEGNTK

FIGURE 10B

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SEQ ID NO: 6	A33_hum	1	W V G K H W P V L W T L C A V R V T V D A I S V E T P Q D V L R A S Q G K S V T L
SEQ ID NO: 1	40628	1	W G T K A Q V E R K L L C L F I L A I L L C S . L A L G S V T V H S S E P E V R I P E N N P V K L

A33_hum	42	P.C†	YHT	TSSREGI	OWOKLLT	HTERVV	IWPFSSNK	YHGEELYXN	AVS1
40628	49	S.CA	YSSGFS	SSPR...	VEW.	XFDAGDTBLV	C..YNNK.	ITAS.	YEDRVT

A33_hum	92	S N H A E Q S O A S A S I T	I D Q L T	W A D N G T Y E C S V S L M S D	I E G N T K S R V A L L V	P P
40628	90	...	L P T G I T F K S V T R E D I G T Y I	Y U S E E G G . N S Y G E V K Y K L I	V L V P P	

A33_hum	142	S K P E C G I E G E T I G N N I Q L T C O S K E G S P T P Q Y S W K R Y N I L N Q E Q P
40628	133	S K P T V N I P S S A T I G N R A V L T C S E Q D G S P P S E Y T W F K D C I V M P T N P K S T R A

A33_hum	187L A P A S G O P V S L K H - S T D T S G Y Y - I C T S N E E G T O F C N I T Y A Y R S
40628	183	F S N S S Y V L N P T I G E . L V F D P L S A S D T G E Y S C E A R G Y G T P M T S N A Y R M E A

A33_hum	231	P S W N V A L Y V G I A V G V V A A L I I G I I Y C C . C C R A G K D O N T E D K E D A R P N R E
40628	232	V E R N Y G V . . . V A A V L V T I I L G I I V F G I W F A Y S A G H F D A T K K G T S S K K V

A33_hum	280	A	Y E E P P E Q L R E L S R E E E D D Y R O E E O R S T G R E S P D O H L D O
40628	279	I	Y S O P S A R S E G E F K O T S S F L V

SEQ ID NO: 6 A33_hum 1 **M G K W W P V L** W T L C A V R V T V D A I S V E T P A D V L R A S O G K S V T L P C T Y H T S T S
 SEQ ID NO: 2 45416 1 **M G I I L G L L** L G H L T V D I Y G R P I L E V P E S V T G P W K G . D Y N L P C T Y D P L Q G

A33_hum 51 **S R E G L I Q W D K L** L T H T E R V V I W . P F S N K N Y I H G E L Y K N R V S I S N N A E Q S D
 45416 49 **Y T Q V L V K W .** L V Q R G S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H K V . P G D

A33_hum 100 **A S I T I D O L T** H A D N G T Y E C S V S . L M S D L E G N T K S A V R I L V Y L V P P S
 45416 96 **V S I Q L S T L E** M O O R S H Y T C E V T W Q T P D G N Q V V R D K I T E L R V O K L S V S K P T V

A33_hum 143 **K P E C G I E G E T I I G N N I Q L T C Q S K E G S P T P Q Y S W K R Y N I L N Q E O P L A O P A S
 45416 146 **T T G S G Y G F T V P Q G** F T V P Q G W A I S L o c a A R . G S P P I S Y I W . . Y K Q Q T N N Q E P I K V A T**

A33_hum 193 **G Q P V S L K N I S T D T** S G Y I C T S S N E E G T . Q F C N I . T V A V A S P S M N V A L Y V G
 45416 193 **L S T L L F K P A V I A D S G S Y F C T A X G Q V G S E O H S D I V K F V V K D O S S K L L K T K T E**

A33_hum 241 **I A V G V V A A L** I I I G I I I Y C C C C R G K D D O N T E D K E D A R P N R E A Y E E P P E O L R E
 45416 243 **A P T T W T Y P L** K A T S T V K O S W D W T T D W D G Y L G E T S A G P G X S L P V F A I I I I S

A33_hum 291 **L S R E R E E E D D Y R Q E E Q R S T G R E** E S P D H L D Q
 45416 293 **L C C M V V F T W A Y I M L C A K T S Q Q E H V Y E A R**

SEQ ID NO: 6 A33_hum 1 . . . M V G K M W P V L W T [CAV R V T V D . . . A I S V E T P Q D V Y L R A S Q G K S V T L P C
SEQ ID NO: 9 35638 1 M A R S R H A L L L L R Y L V V A L G Y H K A Y G F S A P K D Q A V V T A V E Y Q E A I L A C

A33_hum 44 T Y H T S T S R E G L I Q W O K L L T H T E R V Y I W P F S N K N Y I H G E L Y K N R V S I S N
35638 51 . . . K T P K K T V S S R L E W K K L . . . G R S V S F V Y Y Q Q T . L Q G D . F K N R

A33_hum 94 N A E Q S D A S I T D O L T W A D N G T Y E C S V S L M S D L E G N . T K S R Y R L L V L V P P S
35638 87 . A E M I D F N I D R I K N V T R S D A G K Y R C E V S A P S E Q G A N L E E D T Y T L E V L V A P A

A33_hum 143 K P E C G I E G E T I I G N N I Q L T C O S S P T P O Y S W K A Y N I L N O E Q P L A Q P A S
35638 136 V P S C E V P S S A L S G T V V E L R C O D K E G N P A P E Y T W F K D G I R L L E N P R L G S O S

A33_hum 193 G Q P V S L K N I S T D T S G Y Y I C I S S N E E G T Q F C N I T V A V . . . R S P S M N V A L Y V
35638 186 T N S S Y T M N T K I G T L Q F N T . V S K L D T G E Y S C E A R N S V G Y R R C P G K R M Q V D D

A33_hum 240 G I A V G V V A A L I I G I I I Y C C . . . C C A R G K D D N T E D K E D A R P N R E A Y E E P P E
35638 235 L N I S G I I A V V V A L V I S V C G L G V C Y A Q R K G Y F S K E T S F Q K S N S S S K A T T

A33_hum 287 Q L R E L S A . E R E E E D D Y R Q E E Q R S T G R A E S P D H L D Q
35638 285 M S E N V O W L T P V I P A L W K A A A G G S R G Q E F

SEQ ID NO: 10 jam 1 **W G T E G K A G R K L L F L F T . S M I L G C S L V O G K G S V Y T A Q S D V Q Y P E N E S I K L I C**
 SEQ ID NO: 1 40628 1 **W G T K A Q O V E R K L L C I L F I L A I L L C S L A L G S V T Y H S S E P E V R I P E N N P V K L S C**

jam 50 **T Y S G F S S P R V E W K F V Q G S T T A L V C Y N S O I T A P Y A D R V T F S S S G I T F S S V T**
 40628 51 **A Y S G F S S P R V E W K F D Q G O T T R L V C Y N N K I T A S Y E D R V T F L P T G I T F X S V T**

jam 100 **R K D N G E Y T C M V S E E G G O N Y G E V S I H L T V L V P P S K P T I S V P S S V T I G N R A V**
 40628 101 **R E D T G T Y T C M V S E E G G N S Y G E V K V K L I V L V P P S K P T V N I P S S A T I G N R A V**

jam 150 **L T C S E H D G S P P S E Y S W F K D G I S M L T A D A K K T R A F H N S S F T I O P K S G D L I F**
 40628 151 **L T C S E O D G S P P S E Y T W F K D G I . V W P T N P K S T R A F S N S S Y V L N P T T G E L A E**

jam 200 **O P V T A F O S G E Y Y C O A Q N G Y G T A H R S E A X H M D A V E L N V G G I V A A V L V T L I L**
 40628 200 **O P L S A S D T G E Y S C E A R N G Y G T P H T S N A V R A E A V E R N V G V I V A A V L V T L I L**

jam 250 **L G I L I F G V W F A Y S R G Y F E T T K K G T A P G K K V I Y S O P S T A S E G E F K Q T S S F L**
 40628 250 **L G I L V F G I W F A Y S R G H F D R T K K G T . S S K K V I Y S O P S A R S E G E F K Q T S S F L**

jam 300 **Y**
 40628 299 **Y**

jam	49	C T Y S . . . G F S S P R V E W X F V O G S T T A L V . . . C Y N S O I . T A P Y A D R V T F S .
45416	41	C T Y O P L Q G Y T O V L Y K W L V O R G S O P V T I F L R D S S G D H I O O A K Y Q G R L H V S H

jam	90 S S G I T F S S V T A X D N G E Y T C M V . . . S E E G G O N Y G E V S I H L T V L . V P P .
	45416	91 X V P G O V S I Q L S T L E M D D A S H Y T C E V T W Q T P D G N Q V R D K I T E L R Y O X L S V

jam	132	S K P T I S V P S S V T I G N R A Y L T C S E H D G S P P S E Y S W F K D G I S H M L T A D A
	141	S K P T V T T G S G Y G F T V P Q G W R A I S L O C Q A R . G S P P S I S Y I W Y K C O O T N . . . N O E P
	45416	

jam 228 H . . . H D A V E L N V G G I V A A V L V T L I L G L L I F G . . . V W F A Y S R G Y F E T T K K 455416 227 K F V V K D S S X L K T K T E A P T I M T Y P L K A T S T V K Q S W D W T T D M O G Y L G E T S A

jam	272	G T A P G K K V I Y S S O P S T R S E G E F K A T S S F L Y
45416	277	G P G K S L P V F A I L I I S L C C H V V F T W A Y I M L C R K T S Q Q E H V V Y E A A R

SEQ ID NO: 10	jam	1	W G T E G K A G R K L L F L F T S H I L G S L V Q C K G S V Y T A Q S D V O V . . . P E N E S I K L
SEQ ID NO: 29	35638	1	W A R R S R H A R L L L L R Y L V V A L G Y H K A Y G F S A P X D o o V U T A V E Y Q E A I L
jam	48	TC . T Y S G F S S S P R V E W K F V O G S T T A L V C Y N S Q I T A P Y A D R V T F S S S S G I T F S	
35638	49	A C K T P K K T V S S A L E W K K L . G A S V S F Y Y Q Q T L O G D F K N R A E W I D F N I R I K	
jam	97	S V T R K D N G E Y T C W V S . . E E G G A N Y G E V S I H C T Y L V P P S K P T I S V P S S V T I	
35638	98	N V T R S D A G K Y R A C E V S A P S E Q Q N L E E D T V T L E V L V A P A V P S C E V P S S A L S	
jam	145	G N R A V L T C S E H D G S P P S E Y S W F K D G I S W L T A D A K K T R A F M N S S F T I D P K S	
35638	148	G T V V E L R C Q D K E G N P A P E Y T W F K D G I R L L . E N P R L G S Q S T N S S Y T M N T K T	
jam	195	G O C I F D P V T A F D S G E Y Y C O A O N G Y G I A M R S E A A H M D A V E L N V G G I V A A V L	
35638	197	G T L A F N T V S K L D T G E Y S C E A R N S V G . Y R R C P G K R M O V D D L N I S G I I A A V V	
jam	245	V T L I L L G L L I F G V W F A Y S R G Y F E T T K K G T A P G K K V I Y S O P S T R S E G E F K Q	
35638	246	V V A L V I S V C G l G V C Y A Q A R K G Y F . . . S K E T S F Q K S N S S S K A T T M S E N V Q O W L	
jam	295	T S S F L V	
35638	293	T P V I P A L W K A A A G G S R G Q E F	

FIG.- 17

SEQ ID NO: 6 A33_hum 1 W V G K W W P V L W T . L C A V R V T V D A I S V E T P Q D V L R A S Q G K S V T L P C T
SEQ ID NO: 10 jam 1 W G T E G K A G R A K L L F L F T S M I L G S L V Q G K G S V Y T A Q S D O V Q V P E N E S I K L T C T

A33_hum 45 Y H T S T S S R E G L I Q W D K L L L T H T E R V V I W P F S N K N Y I H G E L Y K N A V S I S N N
jam 51 Y S G F S S P R . . . Y E W . X F V Q G S T T A L V C . . Y N S Q . . I T A P . Y A D R V T F S S .

A33_hum 95 A E Q S D A S I T I D Q L T H A D N G T Y E C S V S L W S D O L E G N T K S R V R L L V L V P P S K P
jam 91 S G I T F S S V T A R K D N G E Y T C H V S E E G G . Q N Y G E V S I H L T V L V P P S K P

A33_hum 145 E C G I E G E T I I G N N I O L T C O S K E G S P T P O Y S W K R Y N I I N Q E Q P L A Q P A S G Q
jam 135 T I S V P S S V T I G N R A V L T C S E H D G S P P S E Y S W F K D G I S M L T A D A X X T R A F W

A33_hum 195 P V S L K N I S T D T S G Y I C T S S N E E G T Q F C N I T V A V R S P S W N V A L
jam 185 N S S F T I D P K S G D L I F D P V T A F D S G E Y Y C A Q N G Y G T A M R S E A A H M D A V E L

A33_hum 238 Y V . G I A V G V V A A L I I G I I I Y C C C C R G K D D N T E D K E D A R P N R E A Y E E
jam 235 N V G G I V A A Y L V T L I I L G L L I F G V W F A Y S R G Y F E . I T K K G T A P G K X V I Y S Q

A33_hum 284 P P E Q L R E L S R E R E E D D Y R Q E E Q R S T G R E S P D H L D Q
jam 284 P S T R A S E G E F K Q T S S F L V

<u>TISSUE</u>	<u>EXPRESSION</u>	<u>TISSUE</u>	<u>EXPRESSION</u>	<u>TISSUE</u>	<u>EXPRESSION</u>
WHOLE BRAIN	+	HEART	++	KIDNEY	+++
AMYGDALA	+	AORTA	+	LIVER	++
CAUDATE NUCLEUS	+	SKELETAL MUSCLE	+	SMALL INTESTINE	++
CEREBELLUM	-	COLON	+++	SPLEEN	++
CEREBRAL CORTEX	+	BLADDER	++	THYMUS	++
FRONTAL LOBE	+	UTERUS	+	PERIPHERAL LEUKOCYTE	+
HIPPOCAMPUS	+	PROSTATE	+++	LYMPH NODE	+
MEDULLA OBLONGATA	+	STOMACH	+++	BONE MARROW	+
OCCIPITAL LOBE	+	TESTIS	++	APPENDIX	+
PUTAMEN	+	OVARY	+++	LUNG	++++
SUSTANTIA NIGRA	+	PANCREAS	++	TRACHEA	++++
TEMPORAL LOBE	+	PITUITARY GLAND	++	PLACENTA	++++
THALAMUS	+	ADRENAL GLAND	++		
NUCLEUS ACCUMBENS	+	THYROID GLAND	++	FETAL BRAIN	+
SPINAL CORD	-	SALIVARY GLAND	+++	FETAL HEART	+
		MAMMARY GLAND	++	FETAL KIDNEY	++
				FETAL LIVER	++
				FETAL SPLEEN	+
				FETAL LUNG	++++

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FIG. 19

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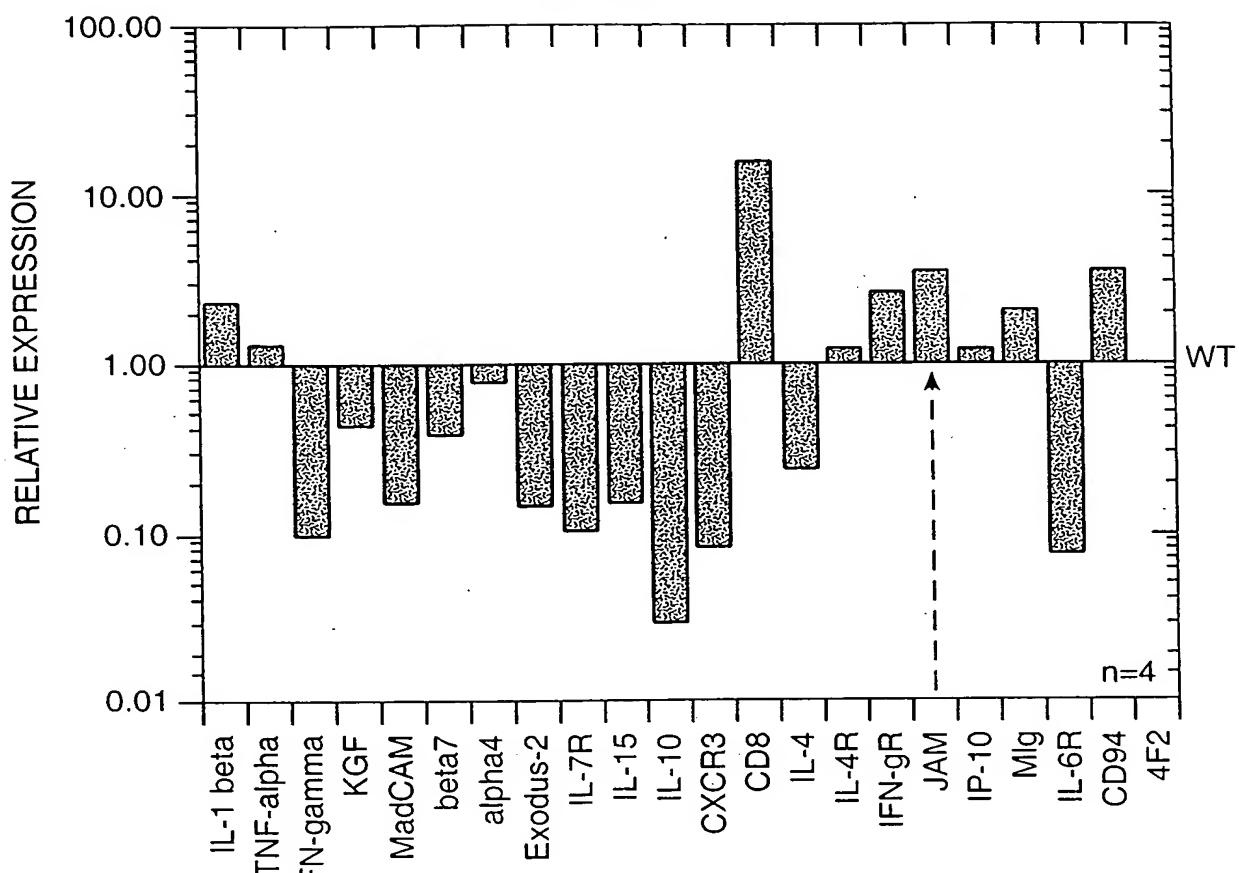


FIG._20

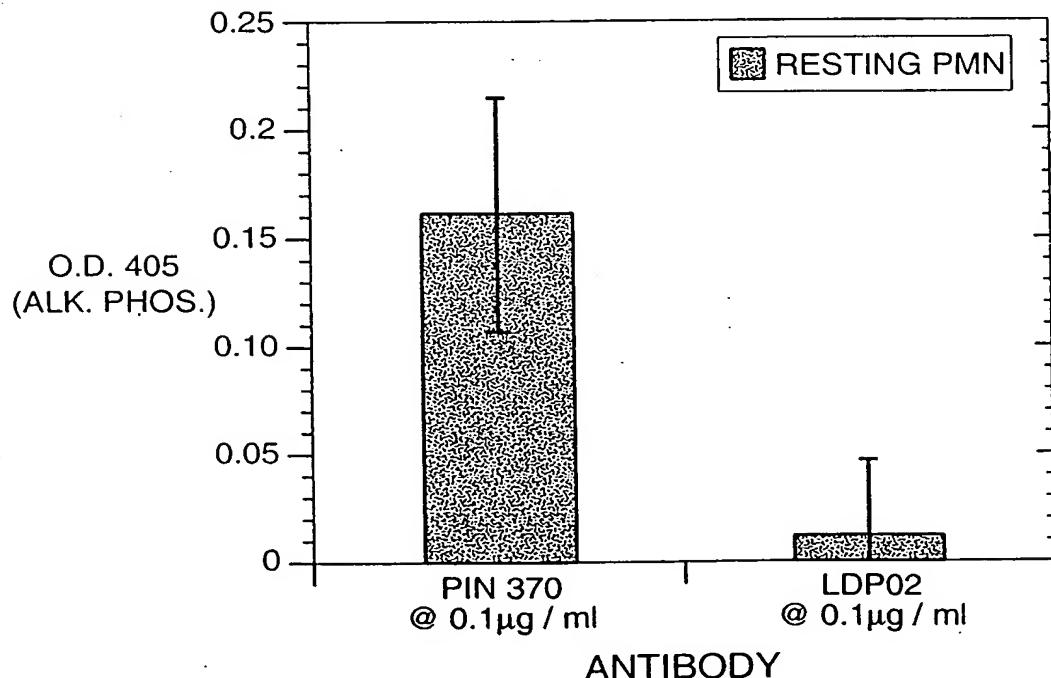


FIG._21